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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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This sequence represents a fragment of the human connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The sequence covers the amino acids encoded by exons 4 and 5 of the full length cDNA sequence (AAAN1280). The protein can be used to raise antibodies which specifically bind to CTFG and are used to treat a CTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and

New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue repair.

Disclosure; Fig 3; 71pp; English.

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Rat CTGF	Rat conne	Rat conne	Porcine c	Bovine co	CTGF prot	Human con	Human con	Human con	-	Human con			Human con	Form proc	Antipsori	Human PRO			Q	Human con

ALIGNMENTS

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Human; connective tissue growth factor; CTGF; mitogen; antibody; liver; fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis; hypertropic scarring; atherosclerosis; diabetic nephropathy; retinopathy; hypertension; cardiovascular disorder; wound healing; bone repair.
                                                                                                                                                                                                                                                                                                                               Human connective tissue growth factor protein fragment.
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14-DEC-1998;
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(FIBR-) FIBROGEN INC.
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DB; AAA11281.
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                                               connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich mitogenic protein which is selectively induced in fibroblasts after activation with transforming growth factor beta (TGF-beta). Recombinant CTGF can be produced in prokaryotic or eukaryotic host cells utilising an isolated CTGF gene (AAT59618). Compsns. comprising CTGF, pref. in combination with TGF-beta, are used to induce bonding formation, e.g. to treat osteoporosis, osteoarchritis and osteochondrytis, to induce tissue and cartilage formation, and to induce wound healing. It can also be used in culture systems e.g. to expand stem cells or chondrocytes prior to reimplantation. CTGF is more stable to protease degradation than other growth factors used as prior art wound healing agents. (Updated on 25-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 172
                             growth factors used 
-2003 to correct PR
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1C1-3; 60pp; English.
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osteoporosis; osteoarthritis; osteochondrytis.
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                                                                          The present invention describes human small CCN-like growth factor (SCGF). SCGF has vulnerary and osteopathic activities, and can be used gene therapy. The SCGF polypeptides and polypucheotides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which given in comparison with the human SCGF in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; small CCN-like growth factor; SCGF; vulnerary; oste gene therapy; muscle wasting disease; osteoporosis; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ctgf CNN family protein sequence SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated polynucleotide sequence encoding a human small CCN-like growth factor, useful for treating muscle wasting disease, and
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                                                                                                                                                                                                                                                                                                                                                                                                             osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HAST/) HASTINGS G A. (ADAM/) ADAMS M D.
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                                                           invention
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                                                                                                                                                                                                                                                                                                                                                    Fig 2A-D; 33pp; English.
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98US-00053587.
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Pred. No. 3.9e-85;
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ound healing;
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Best Local Similarity Matches 172; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Mismatches

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Indels

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Gaps

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Length 348;

Score 956; Pred. No. 3

Query Match Best Local

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Query Match
Best Local S
Matches 172
                                                                               Novel human connective tissue growth factor (CTGF) (AAR79964) is related immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also a chemotactic agent for cells. It is produced by endotherial and fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obtd. by expression of cDNA clone DB60R32 (AAT04226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders associated with overgrowth of cells, such as cancer, fibrotic diseases and atherosclerosis. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connective tissue growth factor; CTGF; wound healing; vulnerary; cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis therapy;
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Modified-site
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12-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5408040-A
                                                                                                                                                                                                                                     Claim 1; Col 19-20; 12pp; English.
                                                                                                                                                                                                                                                                 New connective tissue growth factor - used to develop prods. for wound healing and for diagnosis and therapy of cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                              (UYSF-) UNIV
                                                        Sequence
  Local Similarity
les 172; Conserv
                                                                                                                                                                                                                                                                                                                       1995-161147/21.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= N-glycosylation_site/
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  Score 956; DB 2;
Pred. No. 3.9e-85;
; Mismatches 0;
                            Length 349;
       Indels
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                           This sequence represents the human connective tissue growth factor (CTGF). CTGF is related immunologically and biologically to platelet-CC (ctrived growth factor (PDGF), but is encoded by an unrelated gene. CTGF is thought to play a significant role in the normal development growth, CC and repair of human tissue, similarly to PDGF. The cDNA encoding this CC sequence was isolated by screening a cDNA library from human umbilical CC vein endothelial (HUVE) cells with anti-PDGF antibodies. CTGF can be used CC diagnostic of proliferative diseases involving outgrowth of connective CC diagnostic of proliferative diseases involving outgrowth of connective CC tissue cells, such as cancer, fibrotic disease and atherosclerosis. All CC fitnese diseases can be treated with reagents reactive with CTGF, such as antibodies (which can also serve as assay reagents). Antisense nucleic advantage with using CTGF is that it is more stable, and less susceptible CC droptease degradation than PDGF, and other growth factors involved in CC (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connective tissue growth factor; CTGF; numan; compositive disease; platelet-derived growth factor; PDGF; develop proliferative disease; platelet-derived growth factor; PDGF; develop tissue growth; repair; umbilical vein endothelial cell; HUVE cell; tissue growth; repair; umbilical vein endothelial; atherosclerosis; antibody; wound healing; cancer; fibrotic disease; atherosclerosis; articles, roctease degradation; growth factor; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding connective tissue growth accelerating wound healing, also for diagnosis and proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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14-DEC-1993;
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93US-00167628.
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                                                                                                                                                                                                                                                                                                                                                                                 factor - useful treatment of
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Sequence 349

Length 349;

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Best Local
Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-immunorelated protein that may play a significant role in the normal development, growth and repair of human tissue and probably functions as a growth factor in wound healing. CTGF may be involved in diseases in which there is an overgrowth of connective tissue cells, such as cancer, tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be produced in transformed host cells utilising a cDNA clone isolated from a HUVEC library. It can be used to accelerate wound healing. CTGF
                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                             Connective
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31-MAY-1996;
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26-APR-1997
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Pred. No. 3.9e-85;
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Best Local Sim
Matches 172;
                                                                               A method has been developed for ameliorating a cell proliferative disorder associated with connective tissue growth factor (CTGF). The method comprises the administration of an antibody or its fragment that binds to CTGF and not to platelet-derived growth factor (PDGF), to the site of the disorder. CTGF is related immunologically and biologically to PDGF. The present sequence represents CTGF. The method is used to treat conditions involving the overgrowth of connective tissue cells such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 platelet derived atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                             Ameliorating cell proliferative disorder associated with connective tissue growth factor - comprises the administration of an antibody wibinds to connective tissue growth factor and not to platelet-derived
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Pred.
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No. 3.9e-85;
                                                            diseases
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Length 349;

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RESULT 8
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Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                  30-AUG-1991;
14-DEC-1993;
10-FEB-1995;
02-JUN-1995;
This represents the amino acid sequence of connective tissue growth factor (CTGF). This can be used in the method of the invention for inducing bone or tissue formation that comprises administration to a patient, a composition comprising CTGF and a carrier. CTGF can also be used in a method for inducing wound healing. The methods can be used for inducing wound healing. The methods can be used for inducing bone, tissue or cartilage formation in disorders such as osteoporosis, osteoarthritis or osteochondrytis, arthritis, skeletal disorders, hypertrophic scars, burns, vascular hypertrophy, or in wound healing. The CTGF and functional fragments are more stable and less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wound healing; cartilage formation; osteoporosis; osteoarthritis; burn osteochondrytis; skeletal disorder; hypertrophic scar; protease; PDGF; degradation; vascular hypertrophy; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connective tissue
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                                                                                                                                                      Use of connective tissue growth for cartilage formation in a patient
                                                                                                                                                                                                                                    Grotendorst GR;
                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1998
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                                                                                                                              Disclosure; Fig 1C; 30pp; English.
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DB; AAV65380.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                             SOUTH FLORIDA MIAMI.
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93US-00167628.
95US-00386680.
95US-00459717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "signal peptide" 22. .349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor (CTGF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             "mature protein"
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Pred. No. 3.9e-85;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor; bone formation; tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                     factor -
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                                                                                                                                                        for inducing bone, tis inducing wound healing.
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RESULT 9
AAY18361
ID AAY1
XX AAY1
AC AAY1
XX Huma
XX CTGG
KW CTGGI
KW CTGGI
KW CTGI
XX US5:
XX
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Query Match
Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-1993;
10-FEB-1995;
11-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             susceptible to protease degradation than platelet derived growth factor (PDGF) and other growth factors known to be involved in wound healing
                                                                                                                                             This sequence is the human connective tissue growth factor (CTGF). The invention relates to a method of detecting a cell proliferative disorder comprising comparing the level of CTGF in a sample against a control, where an increase is indicative of a cell proliferative disorder (fibrotic disease or atherosclerosis). The method is used to detect cell proliferative disorders such as fibrotic disease and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                              Detecting cell proliferative disorders such atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGF; connective tissue growth cell proliferative disorder; at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
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                                                                                                Sequence 349
                                                                                                                                                                                                                                                                                                                             Disclosure; Col 15-18; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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nilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grotendorst
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95US-00386680.
96US-00712302.
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Score 956; D
Pred. No. 3.9
0; Mismatches
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Pred. No. 3.9e-85;
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                          956; DB 2;
No. 3.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                              as fibrotic disease
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ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC

Local Sinhes 172;

Similarity

Conservative

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Indels

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Gaps

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RESULT 10

AAY92939

ID AAY92

XX AAY92

XX OB-NO

XX Derma

KW vulne

KW vulne

KW wyoff;

KW myoff;

KW mooff;

KW moof
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                                                                                                                                                                                                 This sequence represents a human connective tissue growth factor (CTGF) polypeptide having the ability to induce extracellular matrix synthesis, collagen synthesis and/or myofibroblast differentiation. The invention relates to fragments of CTGF, especially those encoded by exons 2 and/or 3, which contain the inductive activity. The protein and/or fragments car be used to raise antibodies and the coding sequence can be used to generate antisense oligonucleotides. The antibody or antisense sequence against the CTGF sequence can be used in a method to treat a CTGF associated disease or disorder such as a fibroproliferative disease or disorder, especially selected from kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, angiogenesis related disorders, skin fibrotic
   disorders, and cardiovascular disorders. The disease or disorder can also be selected from acute or repetitive traumas (including surgery or radiation therapy, and fibrosis of organs), diseases caused by vascular endothelial cell proliferation or migration (including cancers), inflammatory bowel disease, Crohn's disease, joint inflammation, interstitial disease, dermatological diseases, diabetes, and keloids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pragment of connective tissue growth factor, useful for treating fibroproliferative diseases or disorders, including kidney fibrosis, scleroderma, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephrotropic; ophthalmological; hypotensive; cardiant; tranquilizer; vulineray; antiinflammatory; human; connective tisues growth factor; CTGF; extracellular matrix synthesis; collagen synthesis; antibody; myofibroblast differentiation; antisense; fibroproliferative disease;
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14-DEC-1998;
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98US-0112241P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                     This sequence represents a human connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The protein can be used to raise antibodies which specifically bind to CTFG and are used to treat i CTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, angiogenesis related disorders, skin fibrotic disorders, and cardiovascular disorders. The protein is also useful in disorders, and cardiovascular disorders. The protein is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                                                                                                                                                                                                                      Grotendorst
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14-DEC-1998;
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 Sequence
                           wound healing,
                                                                                                                                                                             Claim 2,
                                                                                                                                                                                                      mitogenic activity, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension;
                                                                                                                                                                                                       New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue repair.
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                                                                                                                                                                                                                                                                                                                (FIBR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        connective tissue growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            connective tissue growth factor;
                                                                                                                                                                                                                                                                                                                FIBROGEN
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    349
                                                                                                                                                                             3; Fig 2A-B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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                                                                                                                                                                                                                                                                                      GR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disorder; wound healing; bone repair.
                              bone and
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98US-0112241P.
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                              tissue
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Pred. No. 3.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor protein.
                              repair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGF; mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrosis;
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Query Match

100.0%;

Score

956;

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Length

Best Local Similarity

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RESULT 12
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Query Match
Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Connective tissue growth factor; CCN growth factor; beggine; basic fibroblast growth factor; bFGF; neovascular; anothelial cell proliferation; retinal; haemangioma; leukaemia; metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis; endometriosis; Insulin-like growth factor-binding domain; IGF; von Willabrand factor type C repeat; Thrombospondin type 1 domain; von Willabrand factor type C repeat; Thrombospondin type 1
                                                                                                                                                                                                          The present sequence is human connective tissue growth factor, which is a member of CCN growth regulator family. It has antiangiogenic activity and is a potent inhibitor of basic fibroblast growth factor (bFGF) stimulated bovine endothelial cell proliferation. It contains Insulin-like growth factor (IGF)-binding domain, von Willebrand factor type C repeat, Thrombospondin type 1 domain and C-terminal cysteine knot profile (CTCK)-2 domain. It can be used to treat conditions associated with abnormal angiogenesis or neovascularisation like, retinal neovascularisation, tumour growth, haemangioms, solid tumours, leukaemia, metastasis, psoriasis, neovascular glaucoms, diabetic retinopathy, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human connective tissue growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New anti-angiogenic protein containing an IGF binding, Willebrand type C, thrombospondin type I and cysteine knot domains is useful inhibiting atopic angiogenesis e.g. in solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1998;
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                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 26-27; 30pp; English.
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                                                                                                                                                                                    endometriosis and premature retinopathy
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                               100.0%; Score 956; DB 3; 100.0%; Pred. No. 3.9e-85;
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                  The specification describes a pharmaceutical composition, comprising a CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent composition of at least one specific adverse protein, i.e. a composition of the composition are platelet-derived growth factor (PDGF), fibroblast growth factor (FDGF), connective tissue derived growth factor (CTGF), connective macrophage colony stimulating factor (CHC-CSF), connective macrophage colony stimulating factor (CHC-CSF), convention include inhibitors which are included in the composition of the convention include inhibitors of urokinase-type plasminogen activator convention include inhibitors of urokinase, the urokinase composition in useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming growth factor-beta; TGF-beta; matrix metalloproteinase; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor; protein inhibitor; protease; damaged tissue; platelet-derived growth factor; PDGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by arteriosclerosis.
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                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of number of human shear stress response proteins. These are useful diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis a
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                                                                                                                                                                                      Sequence 349
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hypertension
                                                                                                                                                                                                                                                                                                                                                                          Claim 60; Page 460-462; 678pp; Japanese
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Pred. No. 3.9e-85;
Mismatches 0;
                                                                                           Score 956; DB 4;
Pred. No. 3.9e-85;
; Mismatches 0;
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Sugano S;
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178

ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC

ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC

Local Similarity

Conservative

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Indels

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Gaps

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ARBOULT 15
AAB60664
AID AAB60
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Query Match
Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1991;
14-DEC-1993;
10-FEB-1995;
11-SEP-1996;
                                                                                                                                                                                      The invention relates to a method for the recombinant production of human connective tissue growth factor (CTGF; AAB60664), involving transforming a prokaryotic or eukaryotic host cell with an expression construct comprising the CTGF cDNA sequence (AAF59954) or a fragment thereof, and culturing the host cell under conditions suitable for the expression of CTGF. CTGF is a mitogen and chemotactic agent for connective tissue cells and plays a significant role in normal development, growth and repair of human tissues. It is useful as a therapeutic for accelerating wound healing and promoting normal healing mechanisms and may therefore be used in the treatment of e.g., burns. CTGF is also useful as a diagnostic reagent for diagnosing pathological states in a patient suspected of having a disease characterised by a disorder of cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitogenic; chemotactic; tissue development; wound healing; vulnerary; diagnostic agent; cellular proliferation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing connective tissue growth factor involves transforming a cell with polynucleotide encoding the growth factor and growing tunder optimum conditions so that the polynucleotide is expressed.
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                                                                                                               Sequence 349
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DB; AAF59954.
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93US-00167628.
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96US-00712302.
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  Score 956; DB 4;
Pred. No. 3.9e-85;
; Mismatches 0;
                                                                                                                                                                       human CTGF
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Db Search Job tim	ş	DЪ	१
Db 298 TTTLPVEFKCPDGEVMKKNWMFIKTCACHYNCPGDNDIFESLYYKMYGDMA 349 Search completed: January 9, 2006, 11:16:16 Job time : 136 secs	121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172	238 MVRPCEADLEENIKKGKKCIRTPKISKPIKPELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297	61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120

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9.2	9.2	9.3	9.3	9.3	9.4	9.4	9.5	9.5	9.5	9.5	9.5	9.6	9.6	10.1	10.1	10.1	10.4	10.4	10.6	10.7	11.2	12.1	50.2	51.0	54.3	57.2	97.7	100.0	Query
2910	1025	104	2167	1558	1178	388	4006	1372	1042	651	1059	1274	1205	898	654	4753	803	712	807	2098	1444	2165	375	379	357	351	348	349	Length
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otogelin - mouse	secreted Leucine-r	metallothionein-2	hypothetical prote	protein C37C3.6a (thrombospondin pre	circumsporozoite p	probable tenascin	hypothetical prote	mucin SAC (clone L	al prot		cysteine rich prot	procollagen N-endo	hypothetical prote		- 1	F-spondin precurso	immunodominant mic	F-spondin - rat	protein CTRP - mai	11		٠,	gene CYR61 protein	gene novH protein	NOV protein - chic	beta IG-M2 protein	connective tissue	Description

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85	85	85	85	85.5	86	86	86	87	87	87	87	87.5	87.5	87.5	87.5	
8.9	8.9	8.9	8. 9	8.9	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.2	9.2	9.2	9.2	
182	152	152	111	724	1170	951	388	1170	837	732	152	957	442	424	412	
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147105	147112	KRSHHC	T34565	A48569	A40558	T00260	JC6164	TSHUP1	A42112	S47073	I47109	T15976	A54529	A54533	OZZQAF	
high-sulfur wool m	high-sultur wool m	keratin high-sullu	hypothetical proce	antigen Emilo - Ei	thrombospondin i p	hypothetical proce	circumsporozoice p	thrombospondin 1 p	mucin-like peptide	tinger protein HZr	high-sultur wool m	hypothetical proce	circumsporozoice p	circumsporozoice p	circumsporozoite p	

ALIGNMENTS

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RESULT 2
A40578
beta IG-M2 protein precursor - mouse
beta IG-M2 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-***.
C;Accession: A40578; A53228
R;Brunner, A.; Chinn, J.; Mubauer, M.; Purchio, A.F.
RATIONA (Call Biol. 10, 293-300, 1991
A;Title: Identification of a gene family regulated by transforming growth factor-beta.
**Reference number: A40578; MUID:91229699; PMID:2029337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-349 <BRA>
A;Residues: 1-349 <BRA>
A;Coss-references: (WILPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S
A;Cross-references: (WILPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S
R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
A;Description: Differential cloning and expression of human connective tissue growth
A;Reference number: S44205
A;Reference number: S44205
A;Accession: S44205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               connective tissue growth factor - human
(;Species: Homo sapiens (man)
(;Pate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
(;Accession: A40551; S44205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A;Reference number: A40551; MUID:91373462; PMID:1654338
A;Accession: A40551; MUID:91373462; PMID:1654338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-349 <OBM
A;Cresidues: 1-349 <OBM
A;Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934
C;Superfamily: IGFBP-related protein, CNN type
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Best Local Similarity 100.0%; Pred. No. 1e-76;
Matches 172; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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RESULT .
I38069
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A;Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gA;Reference number: A53228; MUID:91363290; PMID:1888698
A;Accession: A53228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene:
C;Superf
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C;Superfami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Accession: S20078
R;JOllot, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, Mol. Cell. Biol. 12, 10-21, 1992
Mol. Cell. Biol. 12, 10-21, 1992
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A;Residues: 1-160,'K',162-348 <RYS>
A;Cross-references: UNIPARC:UPI000003FD12; GB:M70641; NID:g193313; PIDN:AAA37627.1;
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A; Residues: 1-351 <JOL>
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                                                                                                                                                                                                                                                                                                                                                                         :Superfamily: IGFBP-related protein, CNN type
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                                                                                                                                                                                                                                              ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                    MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
                                                                                                                                                                                                                         AMAAYRQEATLGIDVSDSSANCIEQTTEWSACSKSCGMGFSTRVTNRNQQCEMVKQTRLC
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                                                                                                               TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 159
                                                                                                                                                  MMRPCENE-EPSDKKGKKCIQTKKSMKAVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHN
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                                                                                                                                                                                                                                                                                          57.2%; Scu.
59.7%; Pre
---tive 23;
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95.9%;
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                                                                                                                                                                                                                                                                                                                 Score 546.5; DB Pred. No. 1e-40;
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Pred. No. 8.8e-75;
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C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 31-Dec-2004
C;Accession: I38069
R,Martinerie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong Oncogene 9, 2729-2732, 1994
A;Title: Structural analysis of the human nov proto-oncogene and expression A;Reference number: I38069; MUID:94336229; PMID:7520150
A;Accession: I38069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene CYR61 protein precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence revision 18-Nov-1992 #text_change 31-Dec-2004
C;Accession: A35669; 148319; $16446
R;O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Rol. Cell. Biol. 10, 3569-3577, 1990
A;Title: Expression of cyr61, a growth factor-inducible immediate-early gene A;Reference number: A35669; MUID:90287146; PMID:2355916
A;Accession: A35669; MUID:90287146; PMID:2355916
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                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P18406; UNIPARC:UPI0000022DFF; GB:M32490; NID:g192909; PIDN: A;Note: the authors translated the codon GAT for residue 337 as Gln R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F. Nucleic Acids Res. 19, 3261-3267, 1991
Nucleic Acids Res. 19, 3261-3267, 1991
A;Title: Promoter function and structure of the growth factor-inducible immediate early A;Reference number: 148319; MUID:91288203; PMID:2062642
A;Accession: 148319
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                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-379 <RES>
A;Crose-references: UNIPARC:UPI0000022DFF; EMBL:X56790; NID:g50632; PIDN:CAA40109.1;
A;Note: the authors did not translate the codon for residue 108
A;Note: the authors translated the codon GAT for residue 337 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: IGFBP-related protein, CNN type
F;203-250/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-379 < OAB>
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                                                                                                                                                         A; Introns: 21/3; 93/1; 208/1; 279/3
                                                                                                                                                                              A; Gene: CYR61
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Best Local
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99-166/Domain:
                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 TKTIQAEFQCSPGQIVKKPVMVIGTCTCHTNCPKNNEAFLQELELKTTRGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 VRPCEQEPEQPTDKKGKKCLRTKKSLKAIHLQFKNCTSLHTYKPRFCGVCSDGRCCTPHN
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     83; Conserv
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                                                                                                       IGFBP-related protein, (
n: von Willebrand factor
51.0%;
ilarity 49.4%;
Conservative 3
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Pred. No. 2.7e-38;
"" wigmatches 51;
                             Score 487.5; DB 2
Pred. No. 1.7e-35;
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                                                    DB 2;
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                                                          379;
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Mon

81

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A;Reference number: Z19413

A;Reference number: Z19413

A;Accession: T21371

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Gtatus: preliminary; translated from GB/EMBL/DDBJ

A;Gtatus: preliminary; translated from GB/EMBL/DDBJ

A;Ctoss-references: UNIPROT:Q19791; UNIPARC:UPI000007CF95; EMBL:Z69360; PIDN:CAA93287.1;

A;Cross-references: UNIPROT:Q19791; UNIPARC:UPI000007CF95; EMBL:Z69360; PIDN:CAA93287.1;

A;Egjadsty, S.

R;Gajadsty, S.

R;Gajadsty, S.

R;Gajadsty, S.

A;Reference number: Z19949

A;Accession: T24896

A;Reference number: Z19949

A;Accession: T24896

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2165 <WIZ>
A;Cross-references: UNIPARC:UPI000007CF95; EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022;

A;Experimental source: clone T13H10

C;Genetics:
A;Gene: CESP:F25H8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L. proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Title: Identification of a phorbol ester-repressible v-src-inducible A;Reference number: A41428; MUID:89145206; PMID:2537491
A;Accession: A41428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEF-10 protein precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text C;Accession: A41428
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                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F25H8.3 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21371; T24896
R;Gajadaty, S.
R;Gajadaty, S.
R;Gajadaty, S.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19413
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A; Residues: 1-375 <SIM>
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Best Local S
Matches 81
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Pred. No. 8.3e-35;
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A; Cross-references: UNIPROT: Q8MYA8; UNIPARC: UPI0000075CEB;
A; Cross-references: UNIPROT: Q8MYA8; UNIPARC: UPI0000075CEB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T18856; T24653
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A; Introns: 31/1; 52/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19031 A;Accession: T18856
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A;Residues: 1-1444 <WI2>
A;Cross-references: UNIPARC:UPI0000075CEB;
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                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: Z19917
                                                                                                                                                                                                                                                                                                                                                                                                        R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;McMurray, A.
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A; Introns: 25/3;
                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                  A; Experimental source: clone
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                                                                                                                                                                                                   25/3; 70/3;
                                 83
                                                                                              27 TEWSACSKTCGM-GISTR---VTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRT
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PRWSEWSSWSACSCFSLTSTRRRFCQVVDPTVQGFCAGAILEQIPCAPGSC 1182
                                 PKISKPIKFELSGCTSMKTYRAKFCGV---
                                                                SDWSSCSKSCGQDGIQTRQKLCLFNNAECSSYAESRRCKDLPSCSSISSGRTISENGFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --HR-TTTLP----VEFKCPDGEVMKKNMMFIKTC-
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nilarity 21.3%;
Conservative 31
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                                                                                                                                                                                                 96/3; 139/3; 187/1; 234/2; 282/3; 376/2;
                                                                                                                                                11.2%; Score 107; DB 2; 26.1%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                        Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
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Pred. No. 0.037;
1; Mismatches
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                                                                                                                                      Mismatches
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56

protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397

RP - malaria parasite (Plasmodium falciparum) Plasmodium falciparum

T18397

R;Trottein,

Triglia,

T.; Cowman,

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A; Molecule type: mRNA
A; Residues: 1-807 < KLA>
A; Residues: 1-807 < KLA>
A; Residues: 1-807 < KLA>
A; Cross-references: UNIPROT: P35446; UNIPARC: UPI000012AC71; GB: M88469; NID: g204176; PIDN: A; Cross-references: UNIPROT: P3646; UNIPARC: UPI000012AC71; GB: M88469; NID: g204176; PIDN: A; Cross-references: UNIPROT: P3640 plate
A; Note: sequence extracted from NCBI backbone (NCBIN: 90877, NCBIP: 90878)
C; Giperfamily: F-spondin; thrombospondin type 1 repeat homology < THR2>
C; Giperfamily: F-spondin; thrombospondin type 1 repeat homology < THR3>
C; Giperfamily: Thrombospondin type 1 repeat homology < THR4>
C; Giperfamily: Thrombospondin type 1 repeat homology < THR4>
C; Giperfamily: Thrombospondin type 1 repeat homology < THR5>
C; Giperfamily: Thrombospondin type 1 repeat homology < THR5>
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C; Giperfamily: Thrombospondin type 1 repeat homology < THR5
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A38152
F-spondin -
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A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
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A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
immunodominant microneme protein Etp100 - Eimeria tenella
C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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24.7%; Pred. No. 0.20
tive 19; Mismatches
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-712 <TOM>
A;Residues: 1-712 <TOM>
A;Residues: 1-712 <TOM>
A;Residues: 1-715 <TOM
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R;TomLey, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter A;Reference number: A45638; MUID:92131064; PMID:1775171
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A;Residues: 1-803 <RUI:
A;Residues: 1-803 <RUI:
A;Cross-references: UNIPROT:P35447; UNIPARC:UPI000012AC72; GB:L09123; NID:g409244; PIDN:
A;Cysuperfamily: R-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>
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   FKCPDGEVMKKNMMFIKTCACH 149
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                                                                                                                                                  IKKGKKCIRTPKISKPIKFELSGCTSMKTYRA----KFCGVCTDGRCCTPHRTTTLPVE
                                                                             LKDAREKRRSEKIKEDSDGEQYPVCKMKPWTAWTECTKFCGGGIQERFMTVKKRFKSSQF
                                                                                                                                                                                                                           LTEWSYWSECNKSCGKGHMIRTRMITMEPOFGGAVCPETVORKKCRLRKCOKSSGNERRH
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Pred. No. 0.46;
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Pred. No. 0.41;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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27-Jun-1994
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F,1054-1095/Domain: LDL receptor ligand-binding repeat hom F,1101-1138/Domain: LDL receptor ligand-binding repeat hom F,1146-1182/Domain: LDL receptor ligand-binding repeat hom F,1187-123/Domain: LDL receptor ligand-binding repeat hom F,1281-123/Domain: LDL receptor ligand-binding repeat hom F,1270-1307/Domain: LDL receptor ligand-binding repeat hom F,1279-1396/Domain: LDL receptor ligand-binding repeat hom F,1313-1350/Domain: LDL receptor ligand-binding repeat hom F,1319-1396/Domain: LDL receptor ligand-binding repeat hom F,1319-1396/Domain: LDL receptor ligand-binding repeat hom F,1319-1364/Domain: LDL receptor ligand-binding repeat hom F,1319-1364/Domain: LDL receptor ligand-binding repeat hom F,2834-2868/Domain: LDL receptor ligand-binding repeat hom F,2819-2956/Domain: LDL receptor ligand-bi
F;3187-3222/Domain:
F;3586-3623/Domain:
F;3527-3666/Domain:
F;3671-3705/Domain:
F;3709-3746/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: tandem repeat; transmembrane protein

F;53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;93-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;233-257/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;263-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;302-336/Domain: EGF homology <EGF1>
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A;Title: A gene for a low density lipoprotein receptor-related protein A;Reference number: A47437; MUID:93281621; PMID:8506301
A;Accession: A47437
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submitted to the EMBL Data
A;Reference number: Z19439
A;Accession: T21547
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submilted to the EMBL Data Library, July 1992
A;Description: A gene for an LDL receptor-rela
A;Reference number: S27801
A;Accession: S27801
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A;Residues: 1-4753 <70C>
A;Cross-references: UNIPROT:Q04833; UNIPARC:UPI000013C4B5; GB:M96150; NID:g156359;
A;Note: nucleotide sequence not given; translation not complete in this paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDL-receptor-related protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabdites elegans
C;Date: 10-Sep-199 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A47437; $27801; T21547
                                                                                                                                                                                                      F;3006-3044/Domain: I
F;3049-3093/Domain: I
F;3100-3135/Domain: I
F;3140-3174/Domain: I
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;Residues: 1-4753 <YO2>
;Cross-references: UNIPARC:UPI000013C4B5; EMBL:M96150; NID:g156359; PIDN:AAA28105.1;
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ligand-binding repeat homology <LD15>
ligand-binding repeat homology <LD16>
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F;3753-3788/Domain: I
F;3793-3830/Domain: I
F;3833-3871/Domain: I
F;3878-3912/Domain: I
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T29247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid A;Reference number: Z20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Minx, P.; Hawkins, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T29247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F09F9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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F;4092-4130/Domain:
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F;4000-4040/Domain:
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hypothetical protein DKFZp434H204.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14764
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                                                                                                                                                                                                                                                                                                                                  89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1;
                                                                                                                                                                 84 KISKPIKFELS---GCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPV--EFKCPDGEVMKK 138
                                                                                                                                                                                                                               27 TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC---MVRPCEADLEBNIKKGKKCIRTP
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 $R_{,i}Wambutt,\ R_{,i}$ Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

- permanent accession numbers. The new UniProt record may not contain the previous temporary accession number numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

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If you have any questions regarding this information or your results, please contact any STIC searcher

numbers. members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please

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CTGF MOUSE
Q98T08 CHICK
Q86270 BOVIN
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Q91V29 MOUSE
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ec_pr.	138; DOI=10.1083/jcb.1: cr: R.L., Grotendorst. cr: a cysteine-rich m. ls is related to the in the interval of	Created) Last sequence update) Last sequence update) tor (Fragment). (Craniata; Vertebrata; E (Coglires; Primates; Catar toglires, Greenlee W.F.; K.M., Greenlee W.F.; or plasminogen activator	CYR61 RAT QARJ69 TETNG CYR61 MOUSE Q9MTM9 RAT Q66HT5 RAT CYR61 HUMAN GEF10 CHICK Q4ZJF1 CHICK Q4ZJF1 CHICK Q53FA4 HUMAN Q6NRAO BRARE Q6PFL2 BRARE Q6PFL2 BRARE Q4SH80 TETNG ALIGNMENTS PRT; 275 AA.
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Connective tissue growth factor precursor (Hypertrophic chondrocyt specific protein 24).
Name=CTGF; Synonyms=CCN2, HCS24;
Homo sapiens (Human).
Enkaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97207446; PubMed=9054739;
Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy
Marz W., Rupp J., Pech M., Luescher T.F.;
"Human connective tissue growth factor is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Umbilical vein endothelial c
MEDLINE-93187114; PubMed=1293144;
Igarashi A., Bradham D.M., Okochi H
"Connective tissue growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;
"Connective tissue growth factor: a cysteine-rich mitogen secreted human vascular endothelial cells is related to the SRC-induced immediate early gene product CBIP 10.";
                                                                  TISSUE=Liver;
Dai W.-J., Ji
                                                                                                                                                                                                      Li Q.-H., Wang L.-C., Liu L.-D., Dong S.-Z
Wang J., He S.-Q., Dong C.-H., Zhao S.-D.,
"Expression, purification and bio-activity
                                                                                                                                                                                                                                                                                                                                                  atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
TISSUE=Umbilical vein
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                                                                                                                                                                                                                                                                                                                          Circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Aorta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91373462; PubMed=1654338;
                                                                                                                   NUCLEOTIDE
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                                                                                                                                                              factor.";
ced (SEP-2003)
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                       mRNA sequence (FEB-2004) to
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                                                                                                                                                                                                                                                                             SEQUENCE [MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                   SEQUENCE
                                                                       Jiang H.-C.,
                                                                                                                                                                                                                                                                                                                          otic lesions.";
95:831-839(1997).
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114:1285-1294(1991).
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                                                 S.-B.;
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Pred. No. 4.4e-81;
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RA Wilming L. Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Almeida J.P., Ambrose K.D., Bathel G., Milne S., Alinscough R.,
RA Almeida J.P., Ambrose K.D., Bailey J., Banerjee R., Barker D.J.,
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bares K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Blakey S.E., Bray-Allen S., Brook J., Carder C., Carter N.P.,
RA Blakey S.E., Bares N., Burton J., Carder C., Carter N.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Collier R.E., Collinn S.B., Colman L.K., Corby N.R., Corbley V.,
RA Collier R.E., Collinn J.E., Colman L.K., Corby N.R., Corbley V.,
RA Collier R.E., Faulk D.E., Colman L.K., Corby N.R., Corbley V.,
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RA Collier R.E., Faulk D.E., Colman M., Earthrowl M.E.,
RA Gribble S., Griffiths C.G., Griffiths N.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Gribble S., Griffiths C.G., Griffiths N.N.D., Hall R., Holke E.,
RA Humphray S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Humphray S.J., Morte M.J., McCann O.T., McLaren S.J., McLay K.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA Humphray S., Howden M.J., Phillimore B.J.C.T., Phillips S., Plumb R.M.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.M.,
RA Pearce A.J., Steward C.A., Sycamore N., Tanilyn-Hall G., Tester J.,
RA Wastt J.C., Young L., Younger R.M., Bantley D.R., Coulson A.,
RA Hollen R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RA Humphray S.J., Hart S., Shalley D.R., Coulson A.,
RA Humphray S.J., Hart S., Shalley D.R., Coulson A.,
RA 
                                                                                                                                                                                                Tamatani T., Nishida T., Shimo T., Kol
"Effects of CTGF/Hcs24, a product of a
specific gene, on the proliferation and
chondrocytes in culture."
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"Cloning of human full-length CDSs in BD Creator(TM) system vector.":
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Koundinya M., Raphael J., Moreira D.,
Phelan M., Farmer A.,
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                                                    HEPARIN-BINDING, AND CELL ADHESION.

MEDLINE=22442376; PubMede=12553878; DOI=10.1677/joe.0.176R001;

Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;

Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;

"The heparin-binding 10 kDa fragment of connective tissue grofactor (CTGF) containing module 4 alone stimulates cell adhes

J. Endocrinol. 176:R1-R7(2003).
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                                                                                                                                                                                           Endocrinology 141:264-273 (2000).
                                                                                                                                                                                                                                                                                                               TISSUE=Chondrocyte;
MEDLINE=20080284; P
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FUNCTION: Major connective tissue mitoattractant se vascular endothelial cells. Promotes proliferation differentiation of chondrocytes. Mediates heparin-
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                                                                                                                                                                                                                                                                                            PubMed=10614647; DOI=10.1210/en.141.1.264; nida T., Shimo T., Kobayashi K., Kubo T.,
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, Schatten R., Shen B., Henze
, Laber J.;
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RGO; GO:0005575; C:extracellular matrix (sensu Metazoa); TAS.

RGO; GO:0005886; C:plasma membrane; TAS.

RGO; GO:0005520; F:insulin-like growth factor binding; TAS.

RGO; GO:0008544; P:epidermis development; TAS.

RGO; GO:0008611; P:response to wounding; TAS.

RINTERPO; IPR006208; Cys knot.

RINTERPO; IPR006208; Cys knot.

RINTERPO; IPR006867; IGFBP_CNN.

INTERPO; IPR000867; IGFBP_CNN.

INTERPO; IPR000867; IGFBP_LIKE.

RINTERPO; IPR0000867; IGFBP_LIKE.

RINTERPO; IPR0000867; IGFBP_LI.

RPfam; PP00007; Cys knot; 1.

RPfam; PP00007; Cys knot; 1.

RPfam; PP00007; TSP_L; 1.

RPfam; PP00009; TSP_L; 1.

RPfam; PP00009; TSP_L; 1.

RPART; SM00041; CT; 1.

RR SMART; SM00021; IGFBP_rP_CNN; 1.

RR SMART; SM00021; IB; 1.

RR SMART; SM00021; IB; 1.

RR SMART; SM00212; IGFBP_RP_CNN; 1.

RR SMART; SM00212; IGFBP_RP_CNN; 1.

RR PROSITE; PS01185; CTCK_1; 1.

RR PROSITE; PS01185; CTCK_2; 1.

RR P
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EMBL; X78947; CAA55544.1; -; mRNA.
EMBL; AX95801; AAQ95223.1; -; mRNA.
EMBL; AX550024; AAS55639.1; -; mRNA.
EMBL; BT019794; AAV38597.1; -; mRNA.
EMBL; BT019795; AAV38597.1; -; mRNA.
EMBL; BT019795; AAV38597.1; -; mRNA.
EMBL; BT019795; CAG46559.1; -; mRNA.
EMBL; AL354866; CAG44023.1; -; Genomic_DNA.
EMBL; AL354866; CAG44023.1; -; Genomic_DNA.
EMBL; AL354866; CAG44023.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collabout between the Swiss Institute of Bioinformatics and the EMBL outstate European Bioinformatics Institute. There are no restrictions can be along as its content is in no way modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note=No experimental confirmation available;
SIMILARITY: Belongs to the CCN family.
SIMILARITY: Contains 1 CTCK (Crterminal cystine knot-like) domain.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial cells. Enhances fibroblast growth factor-induced DNA synthesis. SUBUNIT: MONOMER: SUBCELLULAR LOCATION: Found in the extracellular matrix and as soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=Short; IsoId=P29279-2; Sequence=VSP_002460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=Long;
IsoId=P29279-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
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  TSP type-1.
CTCK.
Heparin-binding.
N-linked (GlcNAc.
                                                                                    IGFBP.
                                                                                                                              Connective
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Halleck A., Ebert L., Mkoundinya M., Schick M., I

Meubert P., Kstrang K., Schatten R., Shen B., Her

KOrn B., Zuo D., Hu Y., LaBaer J.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat

EMBL; CR541734; CA646534.1; -, mRNA.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005520; F:insulin-like growth factor binc

GO; GO:0001558; P:regulation of cell growth; IEA.

RINterPro; IPR006207; Cys knot C.

InterPro; IPR00687; Insl gro_fac_pr.

InterPro; IPR00087; Insl gro_fac_pr.

InterPro; IPR000887; Insl gro_fac_pr.

RINterPro; IPR000887; Insl gro_fac_pr.

RINterPro; IPR001007; WWF C.

R InterPro; IPR001007; WWF C.

R InterPro; IPR001007; WWF C.

R Ffam; PF000219; IGFBP; 1.

R Ffam; PF000219; IGFBP; 1.

R Ffam; PF00093; VWC; 1.

R SMART; SM001214; IB; 1.

R SMART; SM001214; IB; 1.

R SMART; SM001214; IRS. CTCY 1. 1.
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06FHL8;

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CTGF protein.
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PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS00222; IGF BINDING;
PROSITE; PS50092; TSPI; 1.
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Eukaryota; Metazoa; C
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                                                                                                      PS01208; VWFC_1; 1.
PS50184; VWFC_2; 1.
349 AA; 38129 MW;
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Pred. No. 5.6e-81;
Mismatches 0;
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                                                    Score 956; DB 2;
Pred. No. 5.6e-81;
; Mismatches 0;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Roshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

VIllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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Best Local S
Matches 172
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Homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC087839; AAH87839.1; -; mRNA. SEQUENCE 349 AA; 38069 MW; OECF8470B357EA95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Peripheral Nervous
Director MGC Project;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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10-MAY-2005 (TYEMBLRel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
Connective tissue growth factor.
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Q5M8T4;
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c. Natl. Acad. Sci. U.S.A.
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Pred. No. 5.6e-81;
; Mismatches 0;
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RESULT

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O97765_PIG
DO97765_PIG
AC O97765;
AC ON Anne-CTive
GN Name-CTGF;
AC ELKARYOTA;
AC MCBI_TAXID=(
AC MC
   DATE BERNOOS
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STANDARD; PRT; 349 AA.

CTGF BOVIN STANDARD; PRT; 349 AA.

CTGF BOVIN STANDARD;

15-JUL-1998 (Rel. 36, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

10-MAY-2005 (Rel. 47)

10-MAY-2005 (Re
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Best Local
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InterPro; IPR006207; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR000867; Insl gro_fac_pr.
InterPro; IPR000867; Tyspl.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys knot; 1.
Pfam; PF00090; TSP 1; 1.
Pfam; PF00090; TSP 1; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM001214; VWC; 1.
SMART; SM001214; VWC; 1.
SMART; SM001214; VWC; 1.
PROSITE; PS01125; CTCK 2; 1.
PROSITE; PS01125; CTCK 2; 1.
PROSITE; PS01252; TGF BINDING; 1.
PROSITE; PS01253; TGF BINDING; 1.
PROSITE; PS0124; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harding P.A., Brigstock D.R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ
EMBL; U70060; AAD00174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connective tissue growth Name=CTGF;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Eukaryota; Metazoa; Chordata; Crani;
Mammalia; Eutheria; Laurasiatheria;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U70060; AAD00174.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005520; F:insulin-like growth factor
GO; GO:0001558; P:regulation of cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%;
97.7%;
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Pred. No. 9.1e-80;
4; Mismatches 0
                                   Craniata; Vertebrata; Euteleostomi; neria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35AB4275AC1D4B3A CRC64;
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InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot.
InterPro; IPR006207; IGFBP_CNN.
InterPro; IPR012395; IGFBP_LNN.
InterPro; IPR000867; IGFBP_LNN.
InterPro; IPR000867; IGFBP_LNN.
InterPro; IPR000087; VWF_C.
InterPro; IPR001007; VWF_C.
Pfam; PF000097; TSP1; 1.
Pfam; PF000930; TSP1; 1.
Pfam; PF000930; TSP1; 1.
Pfam; PF000930; TSP1; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM001214; VWC; 1.
SMART; SM001214; VWC; 1.
                                                                                                             PROSITE; PS01165; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS001225; IGF BINDING; 1
PROSITE; PS00209; TSPI; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS01204; VWFC 2; 1.
Cell adhesion; DNA symchesis; Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liliensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A.,
Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawroth P.P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
[2]
REGION
DISULFID
DISULFID
DISULFID
DISULFID
CONFLICT
                                                                                              Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913,
                                                                                                                                                                                                                                                                                                            EMBL; AF000137; AAB66596.1; -; mRNA.
EMBL; AF309555; AAG30290.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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325
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VWFC.
TSP type-1.
CTCK.
Heparin-binding ()
By similarity.
By similarity.
By similarity.
By similarity.
D -> DC (in Ref.
                                                                                                Potential
                                                                                      Connective tissue
                                                                                                                Extracellular matrix; Heparin-binding
                                            (By
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                                             Bimilarity).
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                                                                                                                                                                                                                                                                                                PRT; 349.

Jul-1998 (Rel. 36, Created)

Jul-1998 (Rel. 36, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update

Connective tissue growth factor precursor.

V Name=CTGP; Synonyms=CCN2;

Sus scrofa (Pig).

Eukaryota; Metazoa; Chord-

Mammalia; Eutheri-

Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 169
                                                   CONFLICT
                                                                                                                                                                                              "Purification and characterization of novel heparin-binding growth factors in uterine secretory fluids. Identification as heparin-regulated Mr 10,000 forms of connective tissue growth factor."; J. Biol. Chem. 272:20275-20282(1997).
                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                              MEDLINE=97390475; PubMed=9242708; Brigstock D.R., Steffen C.L., Kim
                                                                                                                                                                                                                                            Brigstock D.R., Steffen
                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
         European
as long a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                      P.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAAYRPEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC
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          content is
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98.3%;
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CV -> YI (in Ref. 1).

CDEP -> SRDE (in Ref. 1).

P -> L (in Ref. 1).

L -> Q (in Ref. 1).

C -> Y (in Ref. 1).

B -> Q (in Ref. 1).

C -> Y (in Ref. 1).
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Pred. No. 2.
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           in
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neria; Cetartiodactyla; Suina; Suida
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           g
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G.Y., Vegunta R.
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           way
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2.7e-79;
2;
           modified and
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.K., Diehl J.R.,
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            thie
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                                                                                                                                                                                                                                                                                                                 Suidae;
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                                                                                         Q9RIES; Q9WVS1;

28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 41, Created)
10-MAY-2005 (Rel. 41, Created)
10-MAY-2005 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 41, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
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Pfam; PF00007; Tys knot; 1.
Pfam; PF000219; TSP 1; 1.
Pfam; PF00093; TSP 1; 1.
Pfam; PF00093; VWC; 1.
PIRSF; PIRSF036495; IGFBP_rP_CNN; 1.
SMART; SM00041; CT; 1.
SMART; SM000214; VWC; 1.
SMART; SM000214; VWC; 1.
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Interpro; IPR006207; Cys Knot.
Interpro; IPR012395; IGFBP CNL.
Interpro; IPR010867; IGFBP Like.
Interpro; IPR000867; TSP1.
Interpro; IPR001007; VWF C.
Pfam; PF00007; Cys knot; 1.
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  NUCLEOTIDE SEQUENCE.
MEDLINE=20145935; PubMed=10679821;
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                                                                         NCBI_TaxID=10116;
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; PS00222; IGF BINDING; 1.
; PS50092; TSPI; 1.
; PS50092; TSPI; 1.
; PS01208; VWFC_1; 1.
; PS50184; VWFC_2; 1.
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3.3e-79;
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Pfam; PF00007; CyB knot; 1.
Pfam; PF00009; TSP1; 1.
Pfam; PF00090; TSP1; 1.
Pfam; PF00090; TSP1; 1.
Pfam; PF00093; VWC; 1.
Pfam; PF00093; VWC; 1.
SMART; SM00101; CT; 1.
SMART; SM00101; IB; 1.
SMART; SM0011; VWC; 1.
SMART; SM0011; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS0125; CTCK 2; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS001208; VWFC 1; 1.
PROSITE; PS001208; VWFC 2; 1.
PROSITE; PS001208; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR0012395; IGFBP CNN.
InterPro; IPR001867; IGFBP 1ike.
InterPro; IPR001084; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF000007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Rattus norvegicus connective tissue growth factor.";
Submitted (PEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Major connective tissue mitoattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparinand divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial
  SIGNAL
SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI=10.1002/(SICI)1097-4644(20000401)77:1<103::AID-JCB11>3.0.CO;2-G;
Xu J., Smock S.L., Safadi F.F., Rosenzweig A.B., Odgren P.R.,
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European Bioinformatics
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TSP type-1.
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Best Local &
Matches 165
                                                                          r 01-DEC-1992 (Rel. 24, Created)
r 01-DEC-1992 (Rel. 24, Created)
r 01-DEC-1992 (Rel. 41, Last sequence update)
r 10-MAY-2003 (Rel. 47, Last annotation update)
r 10-MAY-2005 (Rel. 47, Last annotation update)
c Connective tissue growth factor precursor (FISP-12 protometrive tissue growth factor precursor (FISP-12 protometrive tissue growth factor precursor (FISP-12 protometria).
l (Hypertrophic chondrocyte-specific protein 24).
l Name=Ctgf; Synonyms-Ccn2, Fisp-12, Fisp12, Hcs24;
l Name=Ctgf; Synonyms-Ccn2, Hcs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 165;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Connective tissue growth related protein.
Rattus norvegicus (Rat).
Eukarvora. Marian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Connective Tissue Growth Related Gene.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AY596447; AAT08023.1; -; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae; Murinae; Rattus.
                                                            Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.N., Zou Y.L.;
                                                                                                                                                                                                                                                                                                             MOUSE
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Pred. No. 6.3e-79;
5; Mismatches 2
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Pred. No. 6
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6.3e-79;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,
RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Cararinci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Brownstein M.J., Wedin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S.W.,
RA Rodriguez S., Worley A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT and mouse cDNA sequences.";
RT and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RX MEDILINE-99182484; PubMed=10082563;

RA Babic A.M., Chen C.-C., Lau L.F.;

RA Babic A.M., Chen C.-C., Lau L.F.;

RY "Fisp12/mouse connective tissue growth factor mediates endothelial rellatesion and migration through integrin alphaybeta3, promotes gradient almesion and migration through integrin alphaybeta3, promotes related being 19:2958-2966(1999).

RY mol. Cell. Biol. 19:2958-2966(1999).

Mol. Cell. Biol. 19:2958-2966(1999).

Collegion Major connective tissue mitoattractant secreted by concern and differentiation of chondrocytes (By similarity). Mediates heparinand divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial cells (By similarity).

Collagion Similarity).

Collagion Similarity).

Schances fibroblast growth factor induced DNA synthesis (By similarity).

Collagion Similarity).

Collagion Similarity).

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MEDLINE=91229699; Pu
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MEDLINE=97327410; PubMed=9184077; DOI=10.1006/excr.1997.3548;
Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.-C., Ya
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91363290; PubMed=1888698;
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abler A.S., Lau L.F.; "Cyr61 and Fisp12 are both ECM-associated signaling molecules: "cyr61 and Fisp12 are both ECM-associated signaling molecules: "cyr61 and Fisp12 are both ECM-associated signaling molecules: ".";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION
                                                                                                                                                                soluble form.

1. TISSUE SPECIFICITY: Testis, spleen, kidney, (lowest level in testis and highest in lung 1. INDUCTION: By growth factors.

1. SIMILARITY: Belongs to the CCN family.

1. SIMILARITY: Contains 1 CTCK (C-terminal cys 1. SIMILARITY: Contains 1 TSP type-1 domain.

1. SIMILARITY: Contains 1 TSP type-1 domain.

1. SIMILARITY: Contains 1 VWFC domain.
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J., Neubauer M.G.,
f a gene family regn
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regulated by
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a growth factor-
h protein.";
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PIR: A40578; A40578.

REPRINGE A40578; A40578.

REPRINGE A40578; Country of the musculus.

REPRINGE A40578; Cou
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00007; Cyp_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; TSP_1; 1.
Pfam; PF00090; VWC; 1.
PIRSP; PIRSF036495; IGFBP_rP_CNN; 1.
SMART; SM000041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM001214; VWC; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot C.
InterPro; IPR012395; IGFBP CNN.
InterPro; IPR000867; IGFBP like.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF C.
Pfam; PP00007; Cys knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO1208; V
PROSITE; PSO184; V
Cell adhesion; DNA
Signal. 1
CHAIN 26
DOMAIN 26
DOMAIN 10
DOMAIN 197
DOMAIN 197
DOMAIN 255
DISULFID 272
DISULFID 272
DISULFID 272
DISULFID 283
DISULFID 284
DISUL
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PROSITE; PSO1225; CTCK 2; 1.
PROSITE; PSO0222; IGF BINDING; 1.
PROSITE; PS50092; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed
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M70642; AAA37628.1; -; mRNA.
M80263; AAA73135.1; -; mRNA.
    121
                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                    165;
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                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                            MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                       ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGV
                                                                                                                                                                                                                                                     ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFC_1; 1.
VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.7%;
95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37794 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                               5
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TSP type-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 934;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4D7B6D9089174049
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   6.3e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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Best Local S
Matches 164
                                                                                                                                                                                 PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF BINDING; 1
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                            Pfam; PF00007; Cys knot; 1
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; TSP 1; 1.
Pfam; PF00093; VWC; 1.
SMART; SM00021; IB; 1.
SMART; SM000201; TSP1; 1.
SMART; SM00201; TSP1; 1.
SMART; SM00211; VWC; 1.
                                                                                                                      Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by different elements and factors among versions. Chem. 384:1-9(2003).

EMBL; AJ298335; CAC33438:1; -; mRNA.

EMBL; AF463517; AAL68834:1; -; mRNA.

Ensembl; ENSGALG00000002909; Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NÜCLEOTIDE SEQUENCE.
MEDLINE=22984509; PubMed=14623326; DOI=10.1016/j.bbrc.2003.10.061;
Gygi D., Zumstein P., Grossenbacher D., Altwegg L., Luscher T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 30, Last sequence update)
10-MXY-2005 (TrEMBLrel. 30, Last annotation update)
10-MXY-2005 (TrEMBLrel. 30, Last annotation update)
Connective tissue growth factor precursor (Connective tissue growt factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
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28_CHICK
Q98TQ8_CHICK PRELIMINARY;
Q98TQ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GG; GO:0005576; C:extracellular region; IEA.
GG; GO:0008083; F:growth factor activity; IEA.
GG; GO:0005520; F:insulin-like growth factor binding;
GG; GO:0001558; P:regulation of cell growth; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22559415; PubMed=12674494; DOI=10.1515/BC.2003.001; Mukudai Y., Kubota S., Takigawa M.; "Conserved repressive regulation of connective tissue growt factor/hypertrophic chondrocyte-specific gene 24 (ctgf/hcs2 by different elements and factors among vertebrate species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gygi D., Zu
Gehring H.;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human connective tissue growth factor expressed is a non-mitogenic inhibitor of apoptosis."; Biochem. Biophys. Res. Commun. 311:685-690(2003).
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cy8_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                              164;
                                                                            Similarity
                   ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
 ALAAYRLEDTYGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC
                                                                                                                        1
22
344 AA;
                                                                                                                        21
344
37499
                                                                         96.8%;
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                                                            <u>ა</u>
                                                                                                                      Potential.
connective tissue (
69E639AF69BF1D00
                                                           Score 925; DB 2;
Pred. No. 4.3e-78;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     connective tissue growth cific gene 24 (ctgf/hcs24) enabled
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                                                                                                                         growth factor CRC64;
                                                                                         Length 344;
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                                                            Indels
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                                                            Gaps
                                   60
   232
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RESULT 12
O42607 XENLA
ID O42607 X
AC 042607 O1-JAN-1
DT 01-JAN-1
DT 01-FEB-2
DE CONNECTED
CO Xenopodia
OC XENOPODIA
O
RESULT 13
Q505L5 XENLA
ID Q505L5 X
AC Q505L5;
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Best Local S
Matches 156
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InterPro; IPRO06207; Cys knot.
InterPro; IPRO066707; Cys knot.
InterPro; IPRO00867; Insl_gro_fac_pr.
InterPro; IPRO0084; TSP1.
InterPro; IPRO01007; VWF_C.
Pfam; PF00209; IGFBP; 1.
Pfam; PF00209; TSP_1; 1.
Pfam; PF00093; VWC; 1.
SMART; SM000041; CT; 1.
SMART; SM000121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01128; CTCK_2; 1.
PROSITE; PS01128; CTCK_2; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
SMO0SITE; PS01208; VWFC_2; 1.
SROSITE; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43524; AAB67639.1; -; mRNA.
EMBL; U43523; AAB67638.1; -; Genomic DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0005589; P:regulation of cell growth; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connective tissue growth factor XCTGF.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus; Xenopus.
     Q505L5 XENLA PRELIMINARY;
Q505L5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                292
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                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTVRAKFCGVCTDGRCCTPHR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King M.L.;
                                                                                                                                                                                                                                                                                                                               | MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                              TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKNYGDMA 172
                                                                                                                                                                                                                                                                                               MVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                             ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC
                                                                                                                                                                                   TATLPVEFKCPDGEVMKKNMMFIKTCACHFNCPGDNDIFEAMYYRKMYGDMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 898; DB 2;
Pred. No. 1.4e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93F221C5DB565A81 CRC64;
                                   PRT;
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$\\ \text{PR} \t
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";

Br. Narl RA Scherces.";

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Ctgf protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Gerhard D.S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
EMBL; BC094492; AAH94492.1; -; mRNA.
SEQUENCE 343 AA; 37879 MW; 8F448D73C7774FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richardson P
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                                                                                                                                                            61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                               μ.
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TATLPVEFKCPDGEVMKCMMFIKTCACHFNCPGDNDIFEAMYYRKMYGDMA
                                                       TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                     MVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                 ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC
                                                                                                                                                                                                                                                                                     ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 99:16899-16903(2002).
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1; Mismatches
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RESULT 14
Q5BKN7 XENTR
ID Q5BKN7_XENTR PRELIMINARY;
AC Q5BKN7;
DT 10-MAY-2005 (TrEMBLrel. 30,

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schwintz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schwintz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schalka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human recommended".
                                                                                                                                                                                                                                                                                                                                                                          A Klein S., Gerhard D.S.;

A Klein S., Gerhard D.S.;

EMBL; BCO91005; AAH91005.1; -; mRNA.

R Interpro; IPR006208; Cyg_knot.

R Interpro; IPR006208; Cyg_knot.

R Interpro; IPR006207; Cyg_knot.

R Interpro; IPR000867; InsI gro_fac_br.

Interpro; IPR000867; InsI gro_fac_br.

Interpro; IPR000867; InsI gro_fac_br.

R Interpro; IPR000087; VWF_C.

R Interpro; IPR000097; VWF_C.

R Pfam; PF00007; Cyg_knot; 1.

R Pfam; PF00009; TSP 1; 1.

R Pfam; PF00090; TSP 1; 1.

R Pfam; PF00090; TSP 1; 1.

R Pfam; PF00090; TSP 1; 1.

R PART; SM00121; IB; 1.

R SMART; SM00121; IB; 1.

R SMART; SM00121; VWC; 1.

R SMART; SM00214; VWC; 1.

R SMART; SM00214; VWC; 1.

R PROSITE; PS01185; CTCK_1; 1.

R PROSITE; PS01185; CTCK_2; 1.

R PROSITE; PS01225; CTCK_2; 1.

R PROSITE; PS01226; VWFC_2; 1.

R PROSITE; PS012208; VWFC_2; 1.

R PROSITE; PS01208; VWFC_2; 1.

RR PROSITE; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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232
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MVRPCEADLEENIKKGKKCIRTPKISKPVKFEISGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences.";
l. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                            93.5%;
90.1%;
                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                          Score 894; DB Pred. No. 3.4e 12; Mismatches
                                                                                                                                                                                                                                                DB 2;
3.4e-75;
5;
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Matches 157
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Pfam; PF000219; IGPBp; 1.

Pfam; PF00090; TSP_1; 1.

Pfam; PF00093; VWC; 1.

Pfam; PF00093; VWC; 1.

SMART; SM00121; IB; 1.

SMART; SM00121; TSP; 1.

SMART; SM00214; VWC; 1.

SMART; SM00214; VWC; 1.

PROSITE; PS01185; CTCK 1; 1.

PROSITE; PS01225; CTCK 2; 1.

PROSITE; PS00222; IGP BINDING; 1.

PROSITE; PS00222; TSP1; 1.

PROSITE; PS01208; VWFC 1; UNKNOWN_1.

PROSITE; PS01208; VWFC 2; 1.

SEQUENCE 347 AA; 38098 MW; 3B7E239;
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80 NOTVI
Q9PT80_1
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TISSUB-Forelimb blastema;
TISSUB-Forelimb blastema;
MEDLINE=99033008; PubMed=9813273; DOI=10.1016/S0378-1119(98)00478-8;
Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.;
"Identification of newt connective tissue growth factor as a target or retinoid regulation in limb blastenal cells.";
Gene 22:119-124(1998).
[2]
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GG; GO:0005576; C:extracellular region; IEA.
GC; GO:0008083; F:growth factor activity; IEA.
GC; GO:0005520; F:insulin-like growth factor binding;
GC; GO:0001558; P:regulation of cell growth; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000084; TSPl.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
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                         TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-08-90-054-274-2
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nilarity Conservat	14, Application US/ . 5780263 INFORMATION: HASTINGS, Gre OF INVENTION: Huma OF SEQUENCES: OP PONDENCE ADDRESS: ESSEE: CCRELLA, BY ESSEE: CRELLA, BY ESSEE: CRECHI, STE ET: 6 BECKER FARM TO 7068 OF SEQUENCES: OR UTER: 15M PS/2 MITING SYSTEM: MS-D WARE: WORD PERFECT TAPPLICATION NUMBER: US APPLICATION DATA: ICCATION NUMBER: US ING DATE: 6 June 19 SIFICATION UNDRER: US RENCE/DOCKET NUMBER: US RENCE/DOCKET NUMBER: 3 STRATION OR SEG ID NO. ICE CHARACTERISTICS: 3 STRATION SCIL NUMBER: 201-994-170 STRATION OR SEG ID NO. ICE CHARACTERISTICS: 3 STRATION SCIL NUMBER: 201-994-170 STRATION OR SEG ID NO. ICE CHARACTERISTICS: 3 STRATION SCIL NUMBER: 3 STRATION SCIL NUMBER: 3 STRATION OR SEG ID NO. ICE CHARACTERISTICS: 3 STRATION SCIL NUMBER: 3 STRATION SCIL NUMBER: 3 STRATION ACID NUMBER: 3 STRATION SCIL NUMBER: 3 S	444444750000000000000000000000000000000
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                 RESULT 3
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Best Local Similarity
Matches 172; Conserv
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SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
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COMPUTER READABLE FORM:
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
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PRIOR APPLICATION NUMBER: 1
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CITY: LA JO
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wetherell, Jr. Ph.D., REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: PD
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GENERAL INFORMATION:

APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
APPLICANT: Bradham Jr., Douglas M.,
TITLE OP INVENTION: CONNECTIVE TISSUE GROWT!
NUMBER OF SEQUENCES: 2
CORRESSONDENCE ADDRESS:
ADDRESSES: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400

GROWTH

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Sequence 2, Application US/08459717 Patent No. 5770209
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APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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NAME: Wetherell, Jr. Ph.D., John
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/386,680 FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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)GY: linear
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                                                                                                                     TTTLPVEFKCPDGEVMKKNWMFIKTCACHYNCPGDNDIFESLYYRKWYGDMA 349
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4225 Executive Square, Suite 1400
a Jolla
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HOLECULE TYPE: protein
US-08-459-717-2
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph. D., John W.
REGISTRATION NUMBER: 31.678
REFERRNCE/DOCKET NUMBER: PD-1294
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08712302
Patent No. 5783187
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Best Local Similarity
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 2:
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COUNTRY: US
92037
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OP INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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LENGTH: 349 amino acids
TYPE: amino acid
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TELEPHONE: 619-455-5100
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MEDIUM TYPE: Ploppy
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STREET: """
CITY: La Jolla
"""TE: CA
PRIOR APPLICATION DATA:
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Pred. No. 1.9e-83;
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LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-712-302-2
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Best Local Similarity 100.0%;
Matches 172; Conservative C
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
                                                                                                                                                                                                                                                                                       ZIP: 92037

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di.
COMPUTER: IBM PC
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., J
REGISTRATION UNMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1
TELECOMMUNICATION INFORMATION:
TELEPHAX: 619-455-5110
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
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NAME: Wetherell, Jr. Ph.D.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD
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TELEPHONE: 619-455-5100
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET: ta Jolla
CITY: La Jolla
CTATE: CA
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Pred. No. 1.9e-83
); Mismatches 0
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RESULT 8
US-09-097-179-2
; Sequence 2, Application US/09097179
; Patent No. 6149916
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/054,368
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-054-368-2
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Best Local
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APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
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SEQUENCE CHARACTERISTICS
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LENGTH:
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                                                                                                                                                               TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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                                                                                                                                           TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 956; DB 2;
100.0%; Pred. No. 1.9e-83;
tive 0; Mismatches 0;
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Pred. No. 1.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 349;
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RESULT 9 US-09-054-274-2

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Sequence 2, Application US/09054274
Patent No. 6150101
GENERAL INFORMATION:

APPLICANT: University of South Florida
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham, Jr., Douglass M.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
FILS REFERENCE: 07414/003004
CURRENT APPLICATION NUMBER: US/09/054,274
CURRENT FILING DATE: 1998-04-02

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                                                                                                                                                                                                                                                                Query Match
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ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr. Ph.D., J.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: PD-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                     LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ZIP: 92037
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                                                                                                       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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                     TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                         MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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4225 Executive Square, Suite 1400
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VENTION: CONNECTIVE TISSUE GROWTH FACTOR
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Pred. No. 1.9e-83;
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RESULT 10
US-09-080-715-2
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SEQ ID NO 2
SEQ ID NO 2
SENGTH: 349
TYPE: PRT
ORGANISM: Homo Sapiens
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Patent No. 6190884
GENERAL INFORMATION:
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EARLIER FILING DATE: 1995-02-10
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEO ID NOS: 9
                                                                                                         FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGRERICEJ/DOCKET NUMBER: 31,678
REGRERICEJ/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                         TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
            SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,715
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Spensley Horn Jubas & Lubitz
4225 Executive Square, Suite 1400
                                                                                             619-455-5110
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Pred. No. 1.9e-83;
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APPLICANT: University of South Florida
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham, Jr., Douglass M.
APPLICATION CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
FILE REFERENCE: 07414/003002
CURRENT APPLICATION NUMBER: US/09/056,704
CURRENT FILING DATE: 1998-03-03
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
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• FUGTH: 349
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Best Local Similarity
Matches 172; Conserv
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Sequence 4, Application US/09292036 Patent No. 6358741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09056704
Patent No. 6232064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                     / Match 100.0%; Score 956; DB 2; Local Similarity 100.0%; Pred. No. 1.9e-83; nes 172; Conservative 0; Mismatches 0;
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                                                                                                                                      TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                                             TTTLPVBFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Pred. No. 1.9e-83;
Mismatches 0;
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GENERAL INFORMATION: APPLICANT: FIBROGEN, APPLICANT: SCHMIDT,

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                Matches 172;
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-253-316-26
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APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
FILE REFERENCE: 97-75
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TYPE: PRT
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ORGANISM: Homo sapiens
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                                      TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Pred. No. 1.9e-83;
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Pred. No. 1.9e-83;
); Mismatches 0;
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US-09-142-569-8
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                                                                                            Sequence 2, Application US/09461688 Patent No. 6492129 GENERAL INFORMATION:
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Patent No. 6413735
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 172;
                 APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: FRAGMENTS AND METHODS AND USES
FILE REFERENCE: FIBRO1140-2
CURRENT APPLICATION NUMBER: US/09/461,688
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, V CURRENT APPLICATION DATA APPLICATION NUMBER: US/09/142,569
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TOPOLOGY: linear
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100.0%; Pred. No. 1.9e-83;
ative 0; Mismatches 0;
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Tower, 233
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South Wack
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                          Database
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Gapop 10.0 ,
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956
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                                                                                                                                                                                                                                                                                                                                                                                                                              1867569 segs, 417829326 residues
Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAAYRLEDTFGPDPTMIRA.....PGDNDIFESLYYRKMYGDMA 172
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Copyright (c) 1993 - 2006 Compugen Ltd.
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(without alignments)
624.927 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ,	ហ	4	ω	2	,_	Result No.
956	956	956	956	956	956	956	956	956	956	956	956	956	956	956	956	956	956	956	956,	956	956	956	956	956	956	956	Score
100.0		8	8	8	8	8	8	8	100.0	•	8			•	100.0			100.0					•	100.0	•	100.0	Query Match
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Sequence 26, Appl	e 78,	e 1	e 14,	e 7,	8	e 2,	e 60,	e 3,	æ	e 2	e 55,	4	Sequence 2, Appli	е в,	е 7,	e 4	2	Sequence 2, Appli	e 78,	Sequence 46, Appl	173	e 8,	e 26,	Sequence 4, Appli	e 14,	Sequence 4, Appli	Description

938 98.1 226 5 US-10-617-316-163 938 98.1 324 4 US-10-245-977-5 937 98.0 349 4 US-10-245-977-7 934 97.7 347 4 US-10-245-977-7 934 97.7 347 4 US-10-245-977-7 934 97.7 348 3 US-09-853-6258-15 934 97.7 348 4 US-10-101-040-3 934 97.7 348 4 US-10-103-753-6 934 97.7 348 5 US-10-103-604-15 934 97.7 348 5 US-10-627-604-15 934 97.7 348 5 US-10-627-604-15 934 97.7 348 5 US-10-627-604-15 935 95.7 347 4 US-10-101-040-2	4.5	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	ω 0	29
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4 US-10-245-977-6 4 US-10-245-977-7 4 US-10-245-977-7 4 US-10-390-986-2 4 US-10-464-368-56 3 US-09-853-6258-15 4 US-10-10-10-040-3 4 US-10-10-10-10-10-624-368-54 4 US-10-464-368-54 4 US-10-627-604-15 5 US-10-080-173-2	347	347	348	348	348	348	348	348	348	348	348	347	347	347	349	349	226
US-10-617-316-163 US-10-245-977-6 US-10-245-977-7 US-10-245-977-7 US-10-390-986-2 US-10-464-368-56 US-09-853-6258-15 US-10-101-040-3 US-10-101-040-3 US-10-627-604-15 US-10-627-604-15 US-10-627-604-15 US-10-627-604-15 US-10-101-040-2	4	4	IJ	IJ	4.	4.	4	4	4.	4.	w	4	4	4	4	4	U
	US-10-101-040-2	US-10-080-173-2	US-10-627-604-15	US-10-902-895-6	US-10-627-604-15	US-10-464-368-54	US-10-182-432-6	US-10-245-977-8	US-10-053-753-6	US-10-101-040-3	US-09-853-625B-15	US-10-464-368-56	US-10-390-986-2	US-10-245-977-7	US-10-245-977-6	US-10-245-977-5	US-10-617-316-163
	2, Appli	2, Appli	15, App1	6, Appli	_		6, Appli	8, Appli	6, Appli	3, Appli	15, App1		Z, Appii	', Appli	6, Appli	5, Appii	ddy Ypp

ALIGNMENTS

US-10-658-856-4

GENERAL INFORMATION:

Sequence 4, Application US/10658856 Publication No. US20040092450A1

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APPLICANT: Grotendorst, Gary
APPLICANT: Netf, Thomas
TITLE OF INVENTION: Connective Tissue Growth Factor Fragments and Methods and Uses Ti
FILE REFERENCE: FIBRO1130-2
CURRENT APPLICATION NUMBER: US/10/658,856
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: US/99/461,646
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/112,240
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/112,241
PRIOR APPLICATION NUMBER: 60/112,240
PRIOR APPL
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US-09-853-625B-14
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Sequence 14, Application US/09853625B
Patent No. US20020049334A1
PATENT INFORMATION:
GENERAL INFORMATION: Gregg A. and Adams, Mark D.
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 956; DB 4; Length 172; Best Local Similarity 100.0%; Pred. No. 8.4e-84; Matches 172; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10101040 Publication No. US20020142353A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
               APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian
APPLICANT: SCHMIDT, Brian
APPLICANT: ALLEN, Margaret
APPLICANT: SVENDRUP, Fran
APPLICANT: SVENDRUP, Fran
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS
TITLE OF INVENTION: USE
FILE REFERENCE: FIBRO1100-1
CURRENT APPLICATION NUMBER: US/10/101,040
CURRENT FILING DATE: 1099-04-14
PRIOR APPLICATION NUMBER: 09/292,036
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/853,625B
APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14-May-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/053,587
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELEPHONE: 201-994-1700
APPLICATION NUMBER: US 09/292,036
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172;
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CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: «Unknown»
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; PRIOR FILING DATE: 1999-04-14; PRIOR APELICATION NUMBER: US 09/187,478; PRIOR FILING DATE: 1998-11-06; NUMBER OF SEQ ID NOS: 18; SOFTWARE: PATENTIN VERBION 3.0; SEQ ID NO 4; LENGTH: 349; TYPE: PRT
                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo
US-10-011-859-26
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Publication No. US20020147328A1
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/253,316

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/075,300

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspars, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity nes 172; Conserv
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                                      121
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298
                                                                               238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
                                                                                                       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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                                                                                                                                                                                                                                                                                                                                                                                             349
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FastSEQ for Windows Version 3.0
                                                                                                                                                                                        ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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                       TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237
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TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
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                                                                                                                                                                                                                                            100.0%; Score 956; DB 4; ilarity 100.0%; Pred. No. 1.8e-83; Conservative 0; Mismatches 0;
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RESULT 5
US-10-053-753-8
; Sequence 8, Application US/10053753
; Publication No. US20020150986A1
; GENERAL INFORMATION:

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                                                                                                                                                                                                                                           Sequence 173, Application US/10060036 Publication No. US20030073144A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 172; Conserv
                                                            APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,753
FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
OTHER INFORMATION: "CTGF amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
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COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                         TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
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South Wacker Drive
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-46
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 173
LENGTH: 349
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APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
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                                                                                                                                                                                                                           Matches 172;
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 46
                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ORGANISM: Homo sapiens
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               121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                       238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                              178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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Zhao, Xumei
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Kamatkar, Shubhangi
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100.0%; Pred. No. 1.8e-83;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                           Score 956; DB 4;
Pred. No. 1.8e-83;
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CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-25
PRIOR ELING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR PRIOR DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
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                                                                                                                                                                                                        Sequence 2, Application US/10245977 Publication No. US20030113816A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 172; Conservative
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              APPLICANT: Weitz, Stephen L
APPLICANT: Usinger, William R
APPLICANT: Usinger, William R
INTER OF INVENTION, METHODS OF ASSAYING CONNECTIVE
FILE REFERENCE: FP0812 US
CURRENT APPLICATION NUMBER: US/10/245,977
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR FILING DATE: 2001-09-18
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APPLICANT: Monahan, John E
APPLICANT: Endege, Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
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NUMBER OF SEQ ID NOS: 8
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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Kamatkar, Shubhangi
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                                                                                                                                              TISSUE
                                                                                                                                              GROWTH
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US-10-394-015-4

Sequence 4, Application US/10394015 Publication No. US20030180891A1 GENERAL INFORMATION:

APPLICANT: Young, Paul APPLICANT: Ruben, Ste

Steven M.

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; TYPE: PRT; ORGANISM: Homo sapiens US-10-245-977-2
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TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR FRAGMENTS AND METHODS AND USES THE REFERENCE: FIRRO1140-3
CURRENT APPLICATION NUMBER: US/10/315,568
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 09/461,688
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: US 60/112,240
PRIOR APPLICATION NUMBER: US 60/112,241
PRIOR PRIOR DATE: 1998-12-14
PRIOR DATE: 1998-12-14
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US-10-315-568-2
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Publication No. US20030180300A1
GENERAL INFORMATION:
APPLICANT: FibroGen, Inc.
APPLICANT: Grotendorst, Gary R.
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
                                                  TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Pred. No. 1.8
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Pred. No. 1.8e-83;
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APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131,985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/99/726,295
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1909-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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; ORGANISM: Homo sapiens
US-10-394-015-4
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; TYPB: PRT
; ORGANISM: Homo sapiens
US-10-131-985-7
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CURRENT APPLICATION NUMBER: US/10/394,015
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/325,019
PRIOR FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/088,320
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOPTWARE: PATENTIN Ver. 2.0
LENGTH. 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                Matches 172;
                                                                                                                                                                                                                                     Query Match
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APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Connective Tissue Growth Factor-4
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    TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                          MVR PCEADLEENI KKGKKCIRTPKI SKPIKPELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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Pred. No. 1.8e-83;
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Sequence 8, Application US/10182432

Publication No. US20040022124A1

GENERAL INFORMATION:
APPLICANT: LAU, Lester F., YEUNG, Cho-Yau, and GREENSPAN, Jeffrey A.
TITLE OF INVENTION: CYR61 COMPOSITIONS AND METHODS
FILE REFERENCE: 214448/00029

CURRENT APPLICATION NUMBER: US/10/182,432

CURRENT FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 349

TYPE: PRT
ORGANIAN: Homo sapiens
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US-10-182-432-8
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SOFTWARE: PATENTIN VERSIC
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: US 09/054,363
PRIOR FILING DATE: 1998-04-02
PRIOR PELICATION NUMBER: US 08/459,717
PRIOR PELICATION NUMBER: US 08/459,717
PRIOR APPLICATION NUMBER: US 08/386,680
PRIOR PILING DATE: 1995-02-10
PRIOR FILING DATE: 1995-02-10
PRIOR FILING DATE: 1995-02-10
PRIOR PELICATION NUMBER: US 08/167,628
PRIOR APPLICATION NUMBER: US 07/752,427
PRIOR APPLICATION NUMBER: US 07/752,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10338587A Publication No. US20040005319A1 GENERAL INFORMATION:
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Query Match
Best Local Similarity
Matches 172; Conserv
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TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: USF1100-15
CURRENT APPLICATION NUMBER: US/10/338,587A
CURRENT FILING DATE: 2003-01-07
CURRENT FILING DATE: 2003-01-07
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1991-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA APPLICANT: GROTENDORST, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TTTLPVBFKCPDGEVMKKNMMPIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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     Conservative
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     100.0%; Score 956; DB 4;
100.0%; Pred. No. 1.8e-83;
Mismatches 0;

    Mismatches

                                                   Length 349;
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GENERAL INCOMPALIANCE

APPLICANT: GERBER, HANG-PETER

APPLICANT: GERBER, HANG-PETER

FILE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM

FILE REFERENCE: 09800080-0103

CURRENT APPLICATION NUMBER: US/10/428,487

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/815,153

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PRET HOMO Sapiens

US-10-428-487-44
Search completed: January
Job time : 116 BecB
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US-10-428-487-44
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 956; DB 4; Length 349; Best Local Similarity 100.0%; Pred. No. 1.8e-83; Matches 172; Conservative 0; Mismatches 0; Indels
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November 2005

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applications make up the Published_Applications_Main databases. Newly published applications will appear in the Published_Applications_ New databases: older published

Searches run against Amino Acid Published_Applications produce two sets of results, with the ex Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extension rapbm (Published_Applications_AA_Main) and rapbn (Published_Applications_AA_New) .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

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3: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

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5: /cgn2-6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

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US-11-067-121-14
US-10-821-234-1020
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US-11-094-513A-320
US-11-039-398-12
US-11-039-398-16
US-11-039-398-10
US-11-039-398-10
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US-11-109-157A-18
US-11-109-157A-18
US-11-109-157A-18
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   Sequence 14, Appl Sequence 5, Appl Sequence 5, Appl Sequence 18, Appl Sequence 46, Appl Sequence 46, Appl Sequence 11, Appl Sequence 10, Appl Sequence 16, Appl Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 22, Appl Sequence 26, Appl Sequence 27, Appl Sequence 18, Appl Sequence 18, Appl Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 294, Appl Sequence 594, Appl
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	Sequence 14, Appl	Sequence 30, Appl	1133	, -	Sequence 691, App	Sequence 1068, Ap	-		Sequence 14, Appl	Sequence 556, App	Sequence 53, Appl	Sequence 25, Appl	Sequence 223, App	Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 224, App	Sequence 28, Appl	•	Š

ALIGNMENTS

RESULT 1 US-11-067-121-14 ; Sequence 14, Application US/11067121 ; Publication No. US20050261185A1 ; Publication No. US20050261185A1 ; GENERAL INFORMATION: APPLICANT: Martijn, Cecile APPLICANT: Rondahl, Lena TITLE OF INVENTION: THERAPEUTIC PROTEINS FILE REFERENCE: 18909-002001 ; CURRENT APPLICATION NUMBER: US/11/067,121 ; CURRENT FILING DATE: 2005-02-25 PRIOR APPLICATION NUMBER: US 60/576,445 PRIOR FILING DATE: 2004-06-02 ; PRIOR FILING DATE: 2004-06-02 ; PRIOR PILING DATE: 2004-02-27 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 14 ; LENGTH: 349 US-11-067-121-14 Matches 172; Query Match LENGTH: 34 TYPE: PRT ORGANISM: Homo sapiens Match 100.0%; Score 956; DB 7; Local Similarity 100.0%; Pred. No. 1.3e-88; 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 61 MYRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC Conservative 0; Mismatches 0 Length 349; Indels

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RESULT 2 US-10-821-234-1020

Sequence 1020, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:

APPLICANT: Labat, Ivan APPLICANT: Stache-Crain, Birgit APPLICANT: Andarmani, Susan

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US-10-821-234-1020
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Matches 172;
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1020
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PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Martijn, Cecile
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: THERAPBEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
CURRENT FILING DATE: 2005-02-25
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Methods for Diagnosis and
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TYPE: PRT
ORGANISM: Mus musculus
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Similarity 95.9%;
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Pred. No. 2e-86;
5; Mismatches
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Pred. No. 1.5e-88;
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Sequence 38, Application US/11094519A

Publication No. US20050281810A1

GENERAL INFORMATION:

APPLICANT: BERNSTEIN, Jeanne

APPLICANT: LEVINE, ZURIT

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

FILE REFERENCE: 2786-0140P

CURRENT APPLICATION NUMBER: US/11/094,519A

CURRENT FILING DATE: 2005-03-31

PRIOR APPLICATION NUMBER: US/09/695,293

PRIOR APPLICATION NUMBER: US/09/695,293

PRIOR APPLICATION NUMBER: IL 132558

PRIOR APPLICATION NUMBER: IL 132558

PRIOR APPLICATION NUMBER: IL 132558

PRIOR FILING DATE: 1999-10-25

INUMBER OF SEQ ID NOS: 52
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                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-067-121-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
APPLICANT: Rondahl, Lena
APPLICANT: RONDAHL, Lena
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 165; Conserv
                                                                                                                                                                  Query Match 88.7%;
Best Local Similarity 99.3%;
Matches 151; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/067,121
CURRENT FILLING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                  LENGTH: 32
TYPE: PRT
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                                                                                                            NCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCI
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                      RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 140
                                                                                  DCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCI 230
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RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM
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99.4%;
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Pred. No. 1.4e-85;
1; Mismatches 0,
                                                                                                                                                                                          Score 848; DB 7; Pred. No. 7.2e-78;
                                                                                                                                                                        Mismatches
                                                                                                                                                                        0,
                                                                                                                                                                                                              Length 322
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MFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172

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APPLICANT: BENSTEIN, Jeanne
APPLICANT: LEVINE, ZUTİL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPI
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR APPLICATION NUMBER: US 132558
PRIOR APPLICATION NUMBER: IL 132558
PRIOR APPLICATION NUMBER: IL 132558
PRIOR PILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 52
SOTTWARE: PACENTIN VET. 2.1
SEQ ID NO 46
LENGTH: 74
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-11-094-519A-46
                   APPLICANT: Zhang, Zemin APPLICANT: Zhang, Zemin TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF SAUGHTER STATES OF SAUGHTER SAUGHTE
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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Local Similarity 100.0%; Pred. No. 5.3e-37;
1ee 74; Conservative 0; Mismatches 0;
FILING DATE: 1997-08-26
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                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, Colin K
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                           wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A. Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
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                                                                                                                                                                                                                                                                SEQ ID NO 12
LENGTH: 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Apprendication No.
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                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polymucleotides Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                            ORGANISM: homo sapiens
                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                    Local
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FILING DATE: 1997-09-17
                                                    894 PKPIRRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA 949
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                                                                                                                                  45;
                                                                                                                                                    Similarity
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                                                                                                                                Conservative
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                                                                                                                               ; Score 103.5; DB 7; ; Pred. No. 0.0061; 24; Mismatches 57;
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Pred. No. 4.3e-08;
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; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-8
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                                        Sequence 16, Application US/11039398
Publication No. US20050267297A1
GENERRAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nepomnichy, Boris
APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: LEX-0221-USA
CURRENT PRILING DATE: 2005-01-20
CURRENT FILING DATE: 2005-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT:
                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 10.8%; Score 103.5; DB 7; Local Similarity 22.6%; Pred. No. 0.0062; Cocal Similarity 24; Mismatches 57;
                                                                                                                                                                                                                                                                                                  1060 M----CAAE-PCTGDRSVF 1073
                                                                                                                                                                                                                                                                                                                                                                                        1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              894 PKPIRRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA 949
                                                                                                                                                                                                                                                                                                                                         141 MFIKTCACHYNCPGDNDIF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-----CGEGIQQRQVVCRTNA 999
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Nepomnichy, Boris
Hu, Yi
                                      Hilbun,
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FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US/99/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FRABESEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1235
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US-11-039-398-20
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                                                                                                    ; ORGANISM: homo US-11-039-398-20
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SEQ ID NO 20
LENGTH: 1252
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Publication No. US20050267297A1
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Query Match 10.8%; So
Best Local Similarity 22.6%; Pr
Matches 45; Conservative 24;
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APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE REFERENCE: LEX-0221-USA
CURRENT APPLICATION UNMERR: US/11/039,398
CURRENT FILING DATE: 2005-01-20
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                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
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                                                                                                                                                     TYPE: PRT
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nes 45; Conserv
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Score 103.5; DB 7; Pred. No. 0.0063; 14; Mismatches 57;

Indels

73;

Gaps

11;

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APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT APPLICATION NUMBER: US/09/938,330
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-08-22
PRIOR PRIOR FILING DATE: 2000-09-19
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RESULT 13
US-11-039-398-10
Sequence 10, Application US/11039398
; Publication No. US20050267297A1
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Best Local S
Matches 42
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1213
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                           149 HYNCPGDNDIF 159
                                                                                                                                                                                                                                        109 ------VCTDGRCCTPHRTTTLPV---EFKCPDGEVMKKN--MMFIKTCAC 148
                                                                                                                                                                                                                                                                               950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-----CGEGIQQRQVVCRTNA
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22.0%; Pred. No. 0.0087;
1tive 27; Mismatches 6
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Sequence 18, Application US/11039398;
Publication No. US20050267297A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-039-398-10
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                                                  TITLE OF INVENTION: Novel Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the FILE REFERENCE: LEX-0221-USA CURRENT APPLICATION NUMBER: US/11/039,398 CURRENT FILING DATE: 2005-01-20 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: US 60/227,104 PRIOR APPLICATION NUMBER: US 60/227,104 PRIOR APPLICATION NUMBER: US 60/233,796 PRIOR FILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19 PRIOR PRIOR SEO ID NOS: 26
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APPLICANT: Friddle, (
APPLICANT: Turner, (
APPLICANT: Walke, D.)
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1219
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SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nepomnichy, Boris APPLICANT: Hu, Yi
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Hu, Yi
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Turner, C. Alexander Jr.
Walke, D. Wade
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22.0%; Pred
27;
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Pred. No. 0.0087;
27; Mismatches 6
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108

148

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APPLICANT: Nepomnichy, Boris
APPLICANT: Hu, Yi
INPLICANT: Hu, Yi
ITILE OF INVENTION: Novel Human Proteases and
ITILE OF INVENTION: Polynucleotides Encoding the Same
ITILE OF INVENTION NUMBER: US/11/039,398
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
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; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-22
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.7%; Score 102; DB 7; Length 1249; Best Local Similarity 22.0%; Pred. No. 0.0089; Matches 42; Conservative 27; Mismatches 62; Indels 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/11039398 Publication No. US20050267297A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.7%; Score 102; DB 7; Length 1232; Best Local Similarity 22.0%; Pred. No. 0.0088; Matches 42; Conservative 27; Mismatches 62; Indels 60;
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
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                                                                            1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059
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149 HYNCPGDNDIF 159
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Db 1060 TEPCTGDRSVF 1070

Search completed: January 9, 2006, 11:31:22 Job time : 28 secs